FIG. 1

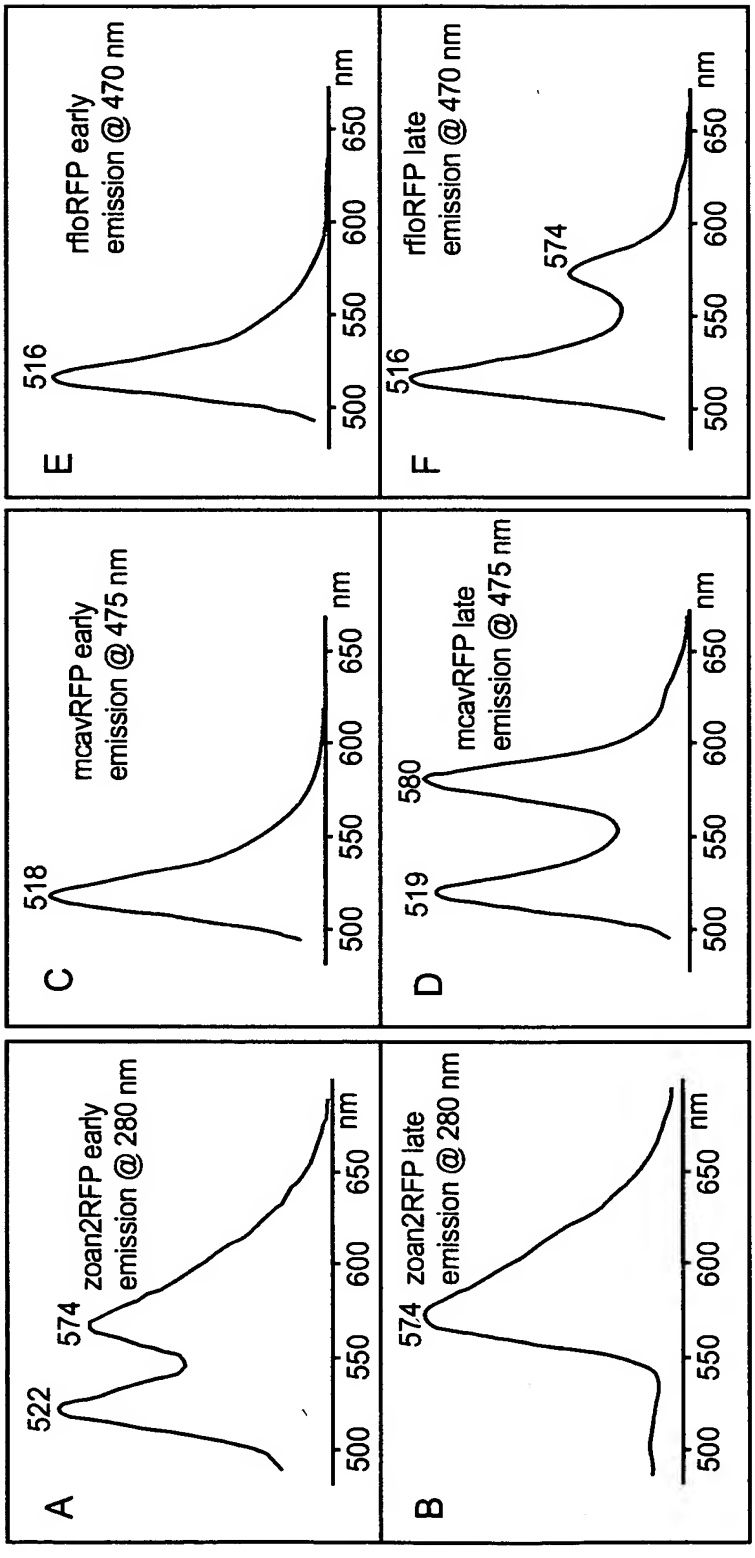


FIG. 2

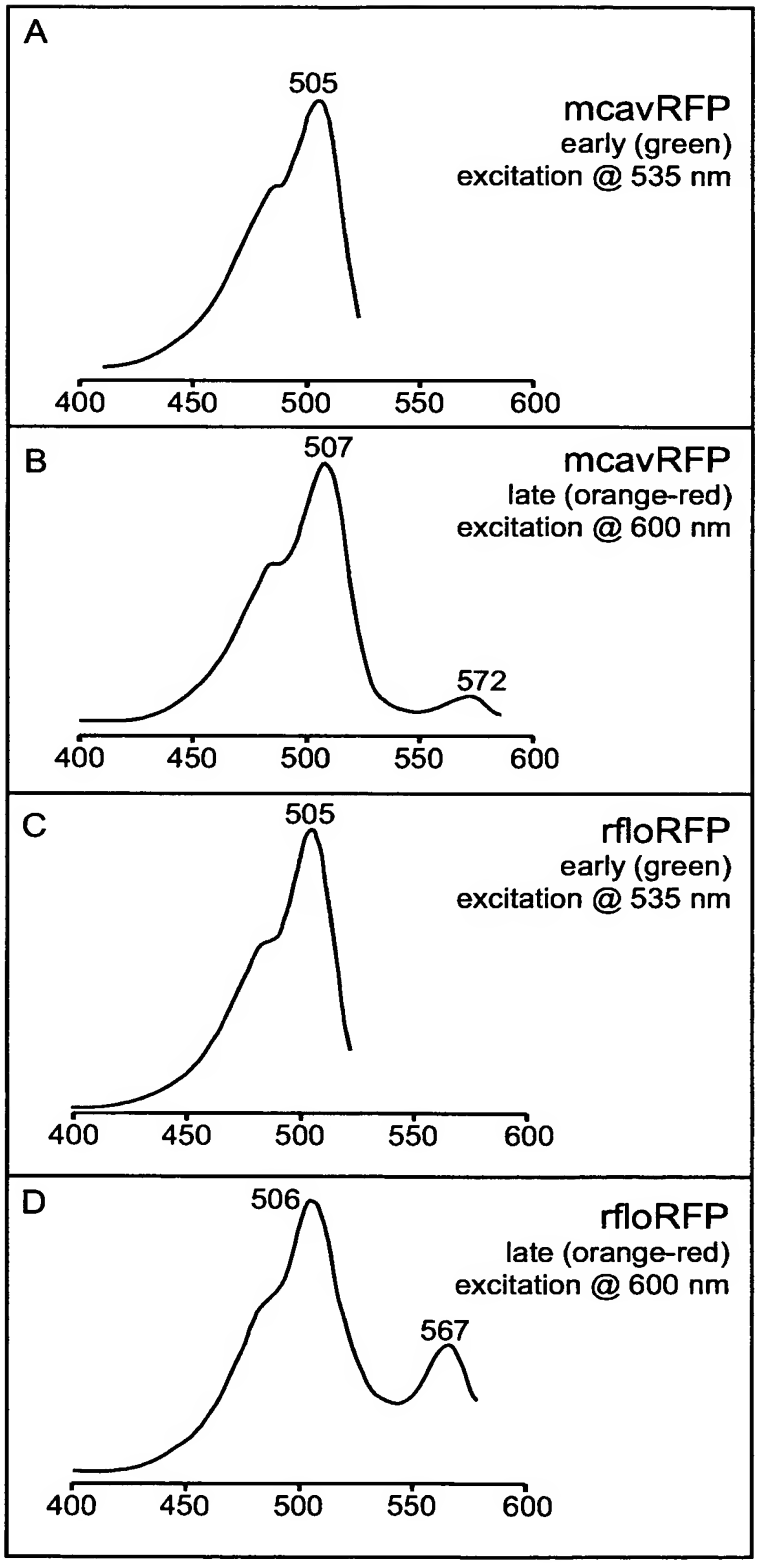

A
505
mcavRFP
early (green)
excitation @ 535 nm
400
450
500
550
600
B
507
mcavRFP
late (orange-red)
excitation @ 600 nm
572
400
450
500
550
600
C
505
rfloRFP
early (green)
excitation @ 535 nm
400
450
500
550
600
D
506
rfloRFP
late (orange-red)
excitation @ 600 nm
567
400
450
500
550
600

FIG. 3

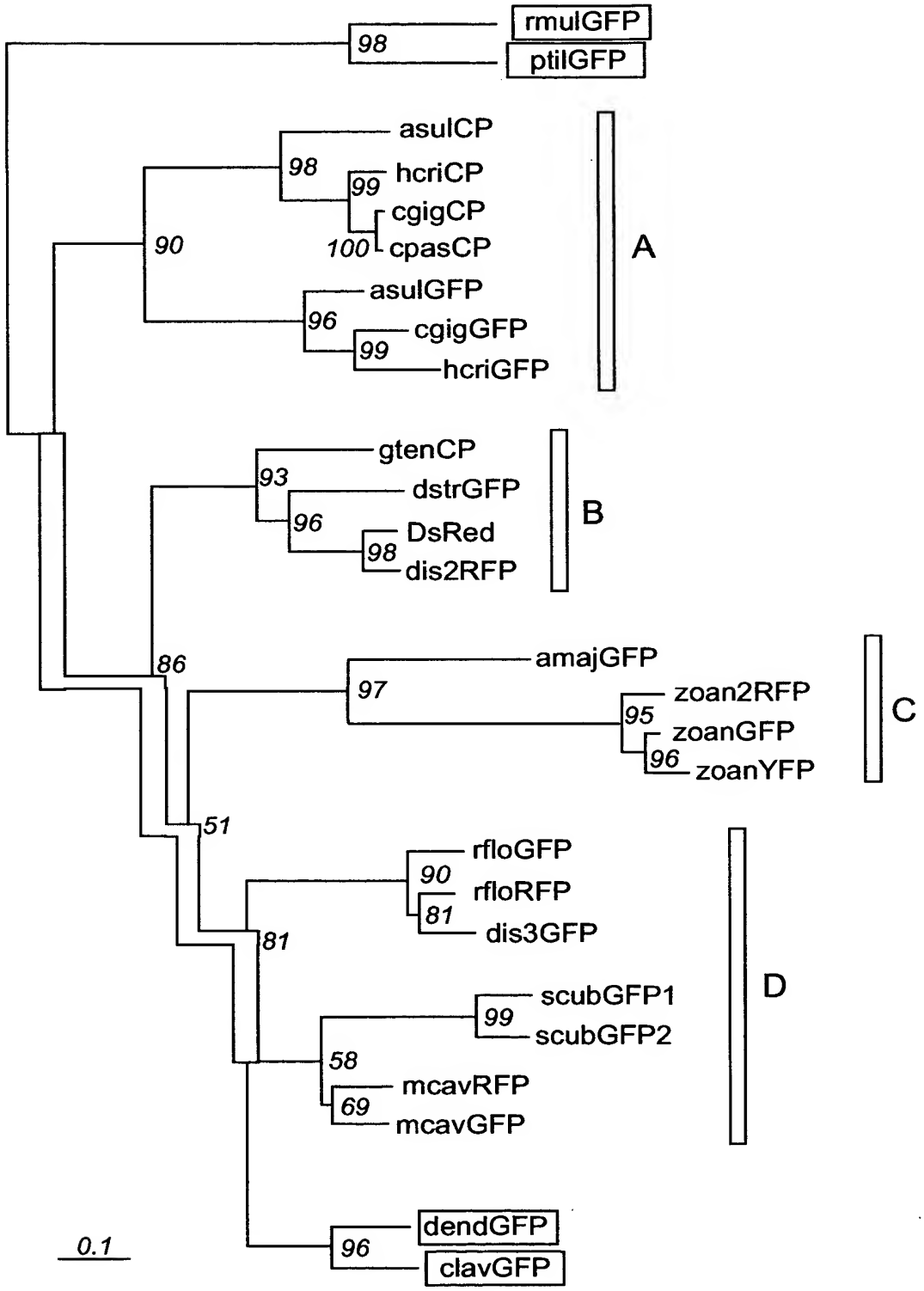

rmulGFP
98
ptilGFP
asulCP
98
hcriCP
99
cgigCP
90
100
cpasCP
A
asulGFP
96
cgigGFP
99
hcriGFP
gtenCP
93
dstrGFP
B
96
DsRed
98
dis2RFP
86
amajGFP
97
zoan2RFP
C
95
zoanGFP
96
zoanYFP
51
rfloGFP
90
rfloRFP
81
dis3GFP
81
scubGFP1
99
scubGFP2
D
58
mcavRFP
69
mcavGFP
dendGFP
96
clavGFP
0.1

FIG. 4A

Protein ID (original ID)	GenBank accession #	Reference
amajGFP (amFP486)	AF168421	2
dstrGFP (dsFP483)	AF168420	2
clavGFP (cFP484)	AF168424	2
GFP	M62653	34
cgigGFP	AY037776	this paper
hcriGFP	AF420592	this paper
ptilGFP	AY015995	35
rmulGFP	AY015996	35
zoanGFP (zFP506)	AF168422	2
asulGFP (asFP499)	AF322221	4
dis3GFP	AF420593	this paper
dendGFP	AF420591	this paper
mcavGFP	AY037769	this paper
rfloGFP	AY037772	this paper
scubGFP1	AY037767	this paper
scubGFP2	AY037771	this paper
zoanYFP (zFP538)	AF168423	2
DsRed (drFP583)	AF168419	2
dis2RFP (dsFP593)	AF272711	36
zoan2RFP	AY059642	this paper
mcavRFP	AY037770	this paper
rfloRFP	AY037773	this paper
asulCP (asCP)	AF246709	3, 4
hcriCP (hcCP)	AF363776	5
cgigCP (cgCP)	AF363775	5
cpasCP (cgCP)	AF383155	5
gtenCP (gtCP)	AF383156	5

FIG. 4B

Taxonomy *Genus species* (Class, Sub-class, Order)
Anemonia majano (Anthozoa, Zoantharia, Actiniaria) *Discosoma striata* (Anthozoa, Zoantharia, Corallimorpharia) *Clavularia sp.* (Anthozoa, Alcyonaria, Alcyonacea)
Aequorea victoria (Hydrozoa,....., Hydroida) *Condylactis gigantea* (Anthozoa, Zoantharia, Actiniaria) *Heteractis crispa* (Anthozoa, Zoantharia, Actiniaria)
Ptilosarcus sp. (Anthozoa, Alcyonaria, Pennatulacea) *Renilla muelleri* (Anthozoa, Alcyonaria, Pennatulacea) *Zoanthus sp.* (Anthozoa, Alcyonaria, Zoanthidea) *Anemonia sulcata* (Anthozoa, Zoantharia, Actiniaria) *Discosoma sp.3* (Anthozoa, Zoantharia, Corallimorpharia) *Dendronephthya sp.* (Anthozoa, Alcyonaria, Alcyonacea) *Montastraea cavernosa* (Anthozoa, Zoantharia, Scleractinia) *Ricordea florida* (Anthozoa, Zoantharia, Corallimorpharia) *Scolymia cubensis* (Anthozoa, Zoantharia, Scleractinia) *Scolymia cubensis* (Anthozoa, Zoantharia, Scleractinia)
Zoanthus sp. (Anthozoa, Zoantharia, Zoanthidea)
Discosoma sp.1 (Anthozoa, Zoantharia, Corallimorpharia) *Discosoma sp.2* (Anthozoa, Zoantharia, Corallimorpharia) *Zoanthus sp.2* (Anthozoa, Zoantharia, Zoanthidea)
Montastraea cavernosa (Anthozoa, Zoantharia, Scleractinia) *Ricordea florida* (Anthozoa, Zoantharia, Corallimorpharia)
Anemonia sulcata (Anthozoa, Zoantharia, Actiniaria)
Heteractis crispa (Anthozoa, Zoantharia, Actiniaria) *Condylactis gigantea* (Anthozoa, Zoantharia, Actiniaria) *Condylactis passiflora* (Anthozoa, Zoantharia, Actiniaria) *Goniopora tenuidens* (Anthozoa, Zoantharia, Scleractinia)

FIG. 4C

Excitation maxima, nm	Emission maxima, nm	Representative spectra excitation —— emission ---------- 400 500 600 nm
458 456 443		458 486 amajGFP A
395, 471 399, 482 405, 481		399 482 496 cgigGFP B
500 498 496 403, 480 503 494 506 508 497 497	508 510 506 499 512 508 515 517 506 506	492 506 zoanGFP C
494, 528	538	zoanYFP 494 528 538 D
558 573 553	583 593 574	zoan2RFP 553 574 E
507, 572 506, 567	519, 580 516, 574	mcavRFP 507 519 580 F
568	none	absorbance only (asulCp) 568
578 571 571 580	none none none none	400 500 600 nm G

FIG. 4D

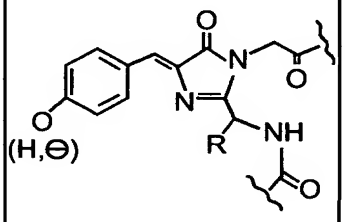
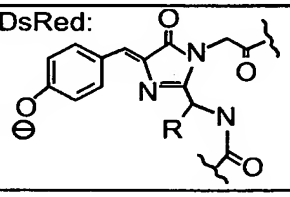
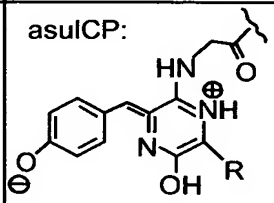
color	Representative chromophore structure
GREEN	GFP: 
YELLOW	?
ORANGE-RED	DsRed: 
	?
PURPLE-BLUE	asulCP: 
	?

FIG. 5

Table 2

clade	colors	Zoantharia orders
A	Green, purple-blue	Actiniaria
B	Green, orange-red, purple-blue	Corallimorpharia, Scleractinia
C	Green, yellow, orange-red	Actiniaria, Zoanthidea
D	Green, orange-red	Corallimorpharia, Scleractinia

FIG. 6

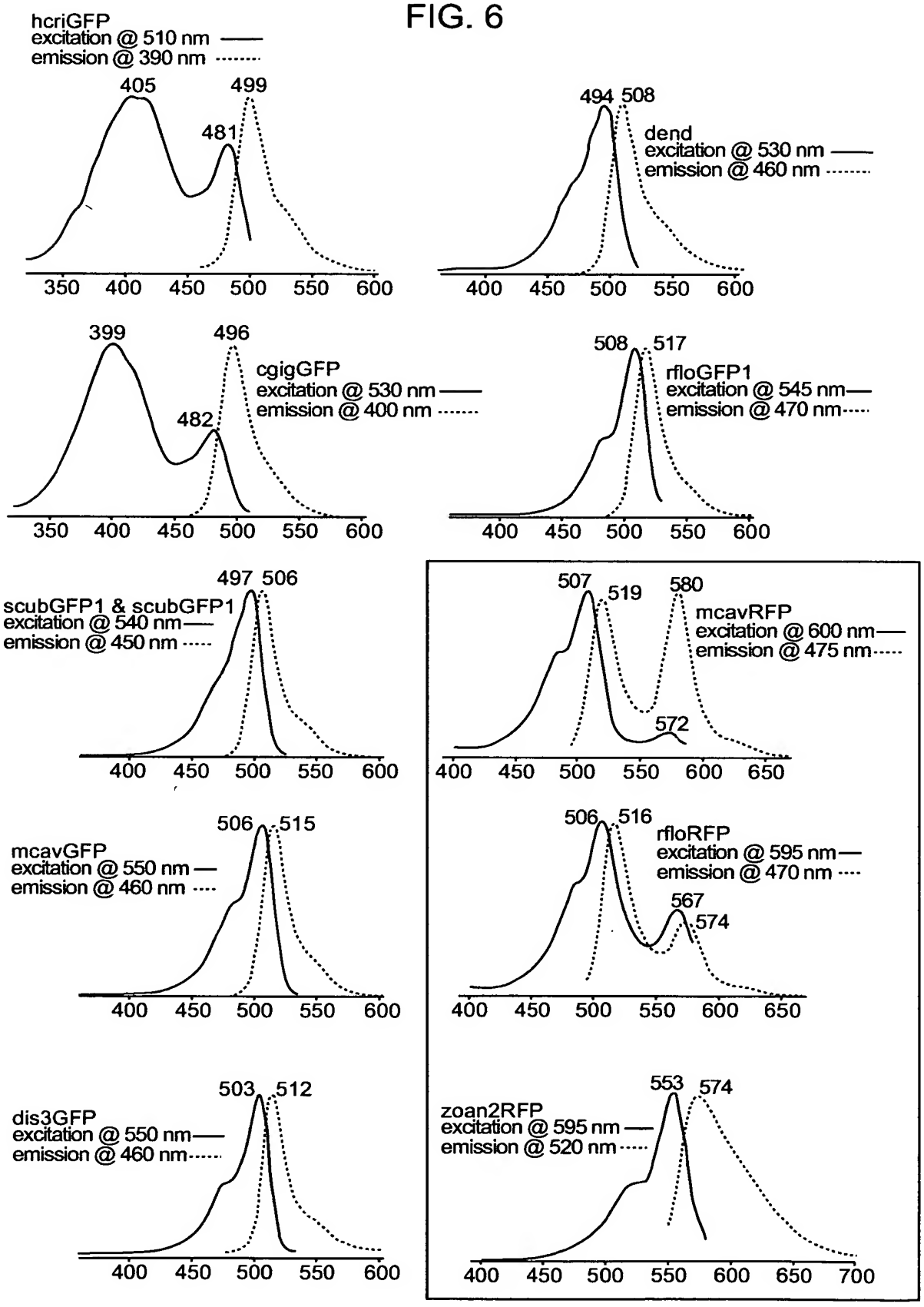

hcriGFP
excitation @ 510 nm
emission @ 390 nm
405
499
481
350 400 450 500 550 600
494 508
dend
excitation @ 530 nm
emission @ 460 nm
400 450 500 550 600
399
496
cgigGFP
excitation @ 530 nm
emission @ 400 nm
482
350 400 450 500 550 600
508 517
rfloGFP1
excitation @ 545 nm
emission @ 470 nm
400 450 500 550 600
497 506
scubGFP1 & scubGFP1
excitation @ 540 nm
emission @ 450 nm
400 450 500 550 600
507
519
580
mcavRFP
excitation @ 600 nm
emission @ 475 nm
572
400 450 500 550 600 650
506 515
mcavGFP
excitation @ 550 nm
emission @ 460 nm
400 450 500 550 600
506 516
rfloRFP
excitation @ 595 nm
emission @ 470 nm
567
574
400 450 500 550 600 650
503 512
dis3GFP
excitation @ 550 nm
emission @ 460 nm
400 450 500 550 600
553 574
zoan2RFP
excitation @ 595 nm
emission @ 520 nm
400 450 500 550 600 650 700

FIG. 7A

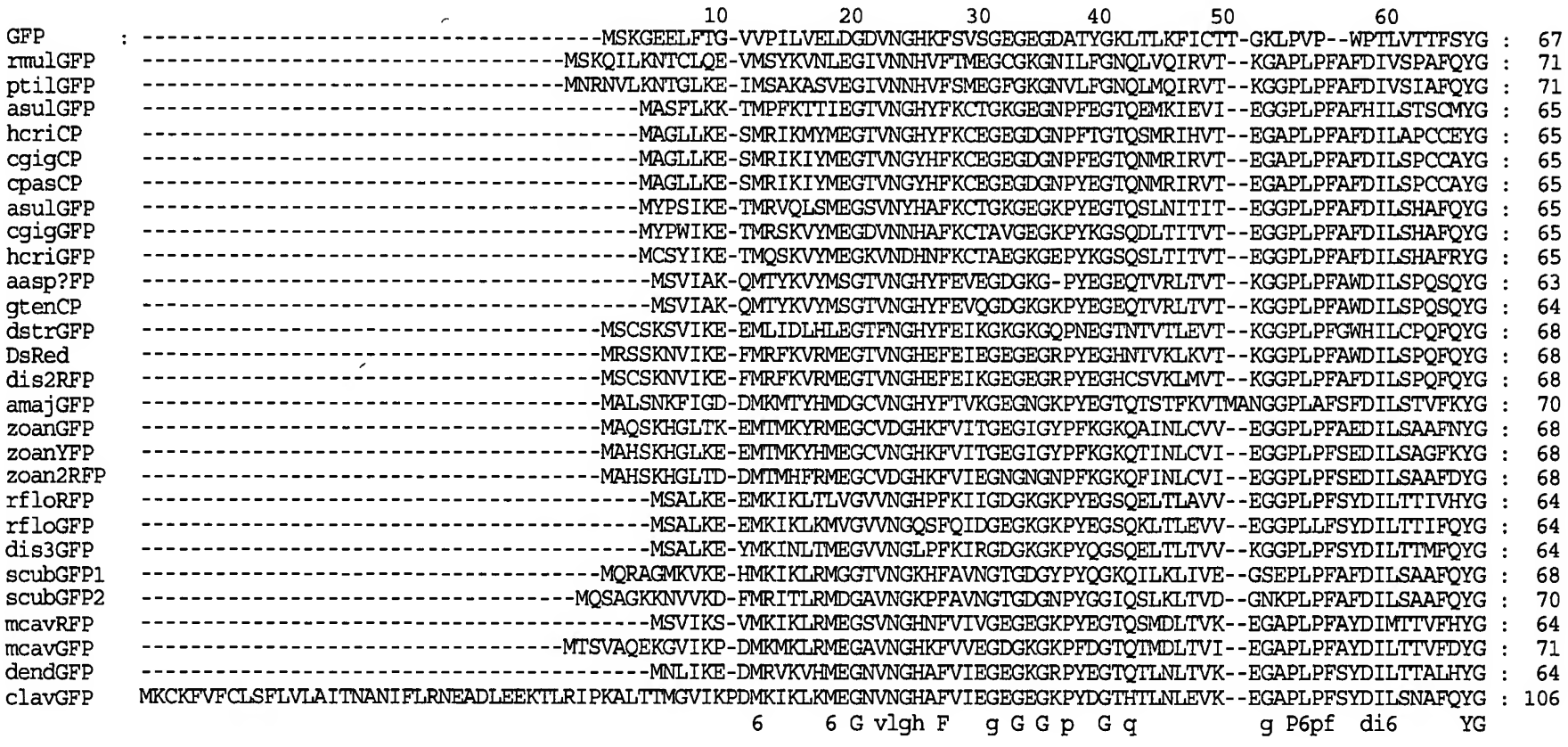

10 20 30 40 50 60
GFP : ----------MSKGEELFTG-VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVP--WPTLVTTFSYG : 67
rmulGFP ----------MSKQILKNTCLQE-VMSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRVT--KGAPLPFAFDIVSPAFQYG : 71
ptilGFP ----------MNRNVLKNTGLKE-IMSAKASVEGIVNNHVFSMEGFGKGNVLFGNQLMQIRVT--KGGPLPFAFDIVSIAFQYG : 71
asulGFP ----------MASFLKK-TMPFKTTIEGTVNGHYFKCTGKGEGNPFEGTQEMKIEVI--EGGPLPFAFHILSTSCMYG : 65
hcriCP ----------MAGLLKE-SMRIKMYMEGTVNGHYFKCEGEGDGNPFTGTQSMRIHVT--EGAPLPFAFDILAPCCEYG : 65
cgigCP ----------MAGLLKE-SMRIKIYMEGTVNGYHFKCEGEGDGNPFEGTQNMRIRVT--EGAPLPFAFDILSPCCAYG : 65
cpasCP ----------MAGLLKE-SMRIKIYMEGTVNGYHFKCEGEGDGNPYEGTQNMRIRVT--EGAPLPFAFDILSPCCAYG : 65
asulGFP ----------MYPSIKE-TMRVQLSMEGSVNYHAFKCTGKGEGKPYEGTQSLNITIT--EGGPLPFAFDILSHAFQYG : 65
cgigGFP ----------MYPWIKE-TMRSKVYMEGDVNNHAFKCTAVGEGKPYKGSQDLTITVT--EGGPLPFAFDILSHAFQYG : 65
hcriGFP ----------MCSYIKE-TMQSKVYMEGKVNDHNFKCTAEGKGEPYKGSQSLTITVT--EGGPLPFAFDILSHAFRYG : 65
aasp?FP ----------MSVIAK-QMTYKVYMSGTVNGHYFEVEGDGKG-PYEGEQTVRLTVT--KGGPLPFAWDILSPQSQYG : 63
gtenCP ----------MSVIAK-QMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVRLTVT--KGGPLPFAWDILSPQSQYG : 64
dstrGFP ----------MSCSKSVIKE-EMLIDLHLEGTFNGHYFEIKGKGKGQPNEGTNTVTLEVT--KGGPLPFGWHILCPQFQYG : 68
DsRed ----------MRSSKNVIKE-FMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVT--KGGPLPFAWDILSPQFQYG : 68
dis2RFP ----------MSCSKNVIKE-FMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVT--KGGPLPFAFDILSPQFQYG : 68
amajGFP ----------MALSNKFIGD-DMKMTYHMDGCVNGHYFTVKGEGNGKPYEGTQTSTFKVTMANGGPLAFSFDILSTVFKYG : 70
zoanGFP ----------MAQSKHGLTK-EMTMKYRMEGCVDGHKFVITGEGIGYPFKGKQAINLCVV--EGGPLPFAEDILSAAFNYG : 68
zoanYFP ----------MAHSKHGLKE-EMTMKYHMEGCVNGHKFVITGEGIGYPFKGKQTINLCVI--EGGPLPFSEDILSAGFKYG : 68
zoan2RFP ----------MAHSKHGLTD-DMTMHFRMEGCVDGHKFVIEGNGNGNPFKGKQFINLCVI--EGGPLPFSEDILSAAFDYG : 68
rfloRFP ----------MSALKE-EMKIKLTLVGVVNGHPFKIIGDGKGKPYEGSQELTLAVV--EGGPLPFSYDILTTIVHYG : 64
rfloGFP ----------MSALKE-EMKIKLKMVGVVNGQSFQIDGEGKGKPYEGSQKLTLEVV--EGGPLLFSYDILTTIFQYG : 64
dis3GFP ----------MSALKE-YMKINLTMEGVVNGLPFKIRGDGKGKPYQGSQELTLTVV--KGGPLPFSYDILTTMFQYG : 64
scubGFP1 ----------MQRAGMKVKE-HMKIKLRMGGTVNGKHFAVNGTGDGYPYQGKQILKLIVE--GSEPLPFAFDILSAAFQYG : 68
scubGFP2 ----------MQSAGKKNVVKD-FMRITLRMDGAVNGKPFAVNGTGDGNPYGGIQSLKLTVD--GNKPLPFAFDILSAAFQYG : 70
mcavRFP ----------MSVIKS-VMKIKLRMEGSVNGHNFVIVGEGEGKPYEGTQSMDLTVK--EGAPLPFAYDIMTTVFHYG : 64
mcavGFP ----------MTSVAQEKGVIKP-DMKMKLRMEGAVNGHKFVVEGDGKGKPFDGTQTMDLTVI--EGAPLPFAYDILTTVFDYG : 71
dendGFP ----------MNLIKE-DMRVKVHMEGNVNGHAFVIEGEGKGRPYEGTQTLNLTVK--EGAPLPFSYDILTTALHYG : 64
clavGFP MKCKFVFCLSFLVLAITNANIFLRNEADLEEKTLRIPKALTTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGEGKPYDGTHTLNLEVK--EGAPLPFSYDILSNAFQYG : 106
6 6 G vlgh F g G G p G q g P6pf di6 YG

FIG. 7B

```
                70        80          90        100       110         120       130       140       150       160
GFP       : VQCFSRYPDHMKQHDFFKSAM---PEGYVQERTIFYKDDGNYKSRAEVKFEGD---TLVNRIELKGIDFKEDGNILGHKMEYNYNSHNVYIMADKQKNGIKVNFKIRH : 169
rmulGFP   : NRTFTKYPNDIS--DYFIQSF---PAGFMYERTLRYEDGGLVEIRSDINLIED---KFVYRVEYKGSNFPDDGPVM-QKTILGIEPSFEAMYM--NNGVLVGEVILVY : 168
ptilGFP   : NRTFTKYPDDIA--DYFVQSF---PAGFFYERNLRFEDGAIVDIRSDISLEDD---KFHYKVEYRGNGFPSNGPVM-QKAILGMEPSFEVVYM--NSGVLVGEVDLVY : 168
asulGFP   : SKTFIKYVSGIP--DYFKQSF---PEGFTWERTTTYEDGGFLTAHQDTSLDGD---CLVYKVKILGNNFPADGPVM-QNKAGRWEPATEIVYE--VDGVLRGQSLMAL : 162
hcriCP    : SRTFVHHTAEIP--DFFKQSF---PEGFTWERTTTYEDGGILTAHQDTSLEGN---CLIYKVKVLGTNFPADGPVM-KNKSGGWEPCTEVVVP--ENGVLCGRNVMAL : 162
cgigCP    : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTTIYEDGGVLTAHQDTSLEGN---CLIYKVKVLGTNFPADGPVM-KKISGGWEPCTEIVYQ--DNGVLRGRNVMAL : 162
cpasCP    : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTTIYEDGGVLTAHQDTSLEGN---CLNYKVKVLGTNFPADGPVM-KNISGGWEPCTEIVYQ--DNGVLRGRNVMAL : 162
asulGFP   : IKVFAKYPKEIP--DFFKQSL---PGGFSWERVSTYEDGGVLSATQETSLQGD---CIICKVKVLGTNFPANGPVM-QKKTCGWEPSTETVIP--RDGGLLLRDTPAL : 162
cgigGFP   : NKVFTDYPDDIP--DFFKQSL---SDGFTWRRVSNYDDGGVLTVTQDTSLKGD---CIICNIKVHGTNFPENGPVM-QNKTDGWEPSTETVIP--QDGGIVAARSPAL : 162
hcriGFP   : NKVFAKYPKDHP--DFFKQSL---PEGFTWERVSNYEDGGVLTVKQETSLEGD---CIICKIKAHGTNFPADGPVM-QKRTNGWEPSTETVIP--RGGGILMRDVPAL : 162
aasp?FP   : SIPFTKYPEDIP--DYVKQSF---PEGYTWERIMNFEDGAVCTVSND-SIQGN---CFIYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMAL : 159
gtenCP    : SIPFTKYPEDIP--DYVKQSF---PEGYTWERIMNFEDGAVCTVSNDSSIQGN---CFIYNVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMAL : 161
dstrGFP   : NKAFVHHPDNIH--DYLKLSF---PEGYTWERSMHFEDGGLCCITNSIDLTGN---CFYYDIKFTGLNFPPNGPVV-QKKTTGWEPSTERLYP--RDGVLIGDIHHAL : 165
DsRed     : SKVYVKHPADIP--DYKKLSF---PEGFKWERVMNFEDGGVVTVTQDSSLQDG---CFIYKVKFIGVNFPSDGPVM-QKKTMGWEASTERLYP--RDGVLKGEIHKAL : 165
dis2RFP   : SKVYVKHPADIP--DYKKLSF---PEGFKWERVMNFEDGGVVTVSQDSSLKDG---CFIYEVKFIGVNFPSDGPVM-QRRTRGWEPSSERLYP--RDGVLKGDIHMAL : 165
amajGFP   : NRCFTAYPTSMP--DYFKQAF---PDGMSYERTFTYEDGGVATASWEISLKGN---CFEHKSTFHGVNFPADGPVM-AKKTTGWDPSFEKMTV--CDGILKGDVTAFL : 167
zoanGFP   : NRVFTEYPQDIV--DYFKNSC---PAGYTWDRSFLFEDGAVCICNADITVSVE-ENCMYHESKFYGVNFPADGPVM-KKMTDNWEPSCEKIIPVPKQGILKGDVSMYL : 169
zoanYFP   : DRIFTEYPQDIV--DYFKNSC---PAGYTWGRSFLFEDGAVCICNVDITVSVK-ENCIYHKSIFNGMNFPADGPVM-KKMTTNWEASCEKIMPVPKQGILKGDVSMYL : 169
zoan2RFP  : NRLFTEYPEGIV--DYFKNSC---PAGYTWHRSFRFEDGAVCICSADITVNVR-ENCIYHESTFYGVNFPADGPVM-KKMTTNWEPSCEKIIPINSQKILKGDVSMYL : 169
rfloRFP   : NRAFVNYPKDIP--DIFKQTCSGPGAGYSWQRTMSFEDGGVCTATSHIRVDGD---TFNYDIHFMGADFPLNGPVM-QKRTVKWEPSTEIMFQ--CDGLLRGDVAMSL : 164
rfloGFP   : NRAFVNYPKDIP--DIFKQTCSGPDGGFSWQRTMTYEDGGVCTASNHISVDGD---TFYYVIRFNGENFPPNGPVM-QKRTVKWEPSTEIMFE--RDGLLRGDIAMSL : 164
dis3GFP   : NRAFVNYPEDIP--DIFKQTCSGPNGGYSWQRTMTYEDGGVCTATSNISVVGD---TFNYDIHFMGANFPLDGPMM-QKRTMKWEPSTEIMFE--RDGLLRGDIAMSL : 164
scubGFP1  : NRAFTEYPTEIA--DYFKQSFEF-GEGFSWERSFTFEDGAICVATNDITMVGG---EFQYDIRFDGLNFPEDGPVM-QKKTVKWEPSTEIMYM--QNGVLKGEVNMAL : 167
scubGFP2  : NRAFTEYPKEIS--DYFKQSFEF-GEGFTWGRSFTFEDGAICVATNDIKMVGD---EFQYNIRFDGVNFPEDGPVM-QKKTVKWEPSTEIMRV--QGGVLKGEVNMAL : 169
mcavRFP   : NRVFAKYPKHIP--DYFKQVF---PEGYSWERSMNFEDGGICTARNEITMEGD---CFFNKVRFDGVNFPPNGPVM-QKKTLKWEPSTEKMYV--RDGVLTGDINMAL : 161
mcavGFP   : NRVFAKYPEDIA--DYFKQTF---PEGYFWERSMTYEDQGICIATNDITMMEGVDDCFAYKIRFDGVNFPANGPVM-QRKTLKWEPSTEIMYA--RDGVLKGDVNMAL : 171
dendGFP   : NRVFTEYPADIT--DYFKQSF---PEGYSWERTMTYEDKGICTIRSDISLEGD---CFFQNIRFNGMNFPPNGPVM-QKKTLKWEPSTEKLHV--RDGLLVGNINMAL : 161
clavGFP   : NRALTKYPDDIA--DYFKQSF---PEGYSWERTMTFEDKGIVKVKSDISMEED---SFIYEIRFDGMNFPPNGPVM-QKKTLKWEPSTEIMYV--RDGVLVGDISHSL : 203
                  yp      D fk      p G    R   5eDg                          G  Fp 1Gp66        ep  e 6      g 6 g     l
```

FIG. 7C

```
          170        180        190        200        210        220        230
GFP       : NIEDG-SVQLADHYQQNTPIGDG-PVLLPDNHYLSTQSALSKDPNEKRDHMILLEFVTAAGITHGMDELYK--------- : 238
rmulGFP   : KLNSG-KYYSCHMKTLMKSKGV--VKEFPSYHFIQHRLEKTYVEDGG--FVEQHETAIAQMTSIGKPLGSLHEWV----- : 238
ptilGFP   : KLESG-NYYSCHMKTFYRSKGG--VKEFPEYHFIHHRLEKTYVEEGS--FVEQHETAIAQLTTIGKPLGSLHEWV----- : 238
asulGFP   : KCPGG-RHLTCHLHTTYRSKKPASALKMPGFHFEDHRIEIMEEVEKGK-CYKQYEAAVGRYCDAAPSKLGHN-------- : 232
hcriCP    : KVGDR--RLICHLYTSYRSKKAVRALTMPGFHFTDIRLQMPRKKKDE--YFELYEASVARYSDLPEKAN----------- : 227
cgigCP    : KVSGR-PPLICHLHSTYRSKK-ACALTMPGFHFADLRIQMPKKKKDE--YFELYEASVARYSDVPEKAT----------- : 227
cpasCP    : KVSGR-PPLICHLHSTYRSKK-ACALTMPGFHFADLRIQMPKKKKDE--YFELYEASVARYSDLPEKAN----------- : 227
asulGFP   : MLADG-GHLSCFMETTYKSKK---EVKLPELHFHHLRMEKLNISDDWK-TVEQHESVVASYSQVPSKLGHN--------- : 228
cgigGFP   : RLRDK-GHLICHMETTYKPNK---EVKLPELHFHHLRMEKLSVSDDGK-TIKQHEYVVASYSKVPSKIGRQW-------- : 229
hcriGFP   : KLLGNKGHLLCVMETTYKSKK---KVNLPKPHFHHLRMEKDSVSDDEK-TIEQHENVRASYFNDSGK------------- : 225
aasp?FP   : KLEGG-GHYLCEFKSTYKAKK---PVRMPGYHYVDRKLDVTNHNKDYT-SVEQCEISIARKPVVA--------------- : 219
gtenCP    : KLEGG-GHYLCEFKSTYKAKK---PVKMPGYHYVDRKLDVTNHNIDYT-SVEQCEISIARKPVVA--------------- : 221
dstrGFP   : TVEGG-GHYACDIKTVYRAKKA--ALKMPGYHYVDTKLVIWNNDKEFM-KVEEHEIAVARHHPFYEPKKDK--------- : 232
DsRed     : KLKDG-GHYLVEFKSIYMAKK---PVQLPGYYYVDSKLDITSHNEDYT-IVEQYERTEGRHHLFL--------------- : 225
dis2RFP   : RLEGG-GHYLVEFKSIYMVKK--PSVQLPGYYYVDSKLDMTSHNEDYT-VVEQYEKTQGRHHPFIKPL------------ : 229
amajGFP   : MLQGG-GNYRCQFHTSYKTKK---PVTMPPNHVVEHRIARTDLDKGGN-SVQLTEHAVAHITSVF-PF------------ : 229
zoanGFP   : LLKDG-GRLRCQFDTVYKAKSV--PRLMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALP--------------- : 231
zoanYFP   : LLKDG-GRYRCQFDTVYKAKSV--PSKMPEWHFIQHKLLREDRSDAKNQKWQLTEHAIAFPSALA--------------- : 231
zoan2RFP  : LLKDG-GRYRCQFDTIYKAKTE--PKEMPDWHFIQHKLNREDRSDAKNQKWQLIEHAIASRSALP--------------- : 231
rfloRFP   : LLKGG-GHYRCDFKTIYKPKK---NVKMPGYHFVDHCIEITSQQDDYN-VVELYEGAVAHYSPLQKPCQAKA-------- : 231
rfloGFP   : LLKGG-GHYRCDFKTIYTPKR---KVNMPGYHFVDHCIEIQKHDKDYN-MAVLSEDAVAHNSPLEKKSQAKA-------- : 231
dis3GFP   : LLKGG-GHYRCDFETIYKPNK---VVKMPDYHFVDHYIEITSQQNYYN-VVELTEVAEARYSSLEKIGKSKA-------- : 231
scubGFP1  : LLQDK-SHYRCDLKTTYKAKNNVP--HPPGYHYVDHCIEILEERKDH---VKLREHAKARSSLSPTSAKERKA------- : 234
scubGFP2  : LLKDK-SHYRCDFKTTYKAKNPVPPTALPDYHYVDHCIEITEENRDY---VNLQEYAKARSGLHLPELQK---------- : 235
mcavRFP   : LLEGG-GHYRCDFRTTYRAKKK--GVKLPDYHFVDHSIEILRHDKEYT-EVKLYEHAEAHSGLPRGQRKA---------- : 227
mcavGFP   : LLEGG-GHYRCDFKTTYKAKK---VVRLPDYHFVDHRIEIVSHDKDYN-KVKLHEHAEARHGLSRKAK------------ : 234
dendGFP   : LLEGG-GHYLCDFKTTYKAKK---VVQLPDYHFVDHRIEILSNDSDYN-KVKLYEHGVARYSPLPKSGLVEVQGKAIMTA : 236
clavGFP   : LLEGG-GHYRCDFKSIYKAKK---VVKLPDYHFVDHRIEILNHDKDYN-KVTLYENAVARYSLL--PSQA---------- : 266
                      c     y  k        P  h                      E   a
```

FIG. 8

Green fluorescent protein from *Heteractis crispa* hcriGFP

```
         10         20         30         40         50         60
ATTTTGGACAGGTGTTCAACCAAGCAAATTTAAGAAGTCATCATCTTTATCTCAGTCAGG

         70         80         90        100        110        120
AAAATGTGTTCTTACATCAAAGAAACCATGCAAAGTAAGGTTTACATGGAAGGAAAAGTT
   M  C  S  Y  I  K  E  T  M  Q  S  K  V  Y  M  E  G  K  V

        130        140        150        160        170        180
AACGACCACAACTTCAAGTGCACTGCAGAAGGAAAAGGAGAACCATACAAAGGCTCACAA
N  D  H  N  F  K  C  T  A  E  G  K  G  E  P  Y  K  G  S  Q

        190        200        210        220        230        240
AGCCTGACGATCACCGTAACTGAAGGAGGTCCTCTGCCATTTGCCTTCGACATTCTTTCA
S  L  T  I  T  V  T  E  G  G  P  L  P  F  A  F  D  I  L  S

        250        260        270        280        290        300
CACGCCTTTCGATATGGCAATAAGGTGTTCGCCAAGTACCCCAAAGATCATCCTGATTTT
H  A  F  R  Y  G  N  K  V  F  A  K  Y  P  K  D  H  P  D  F

        310        320        330        340        350        360
TTTAAGCAGTCTCTTCCTGAAGGTTTTACTTGGGAAAGAGTAAGCAACTATGAGGACGGA
F  K  Q  S  L  P  E  G  F  T  W  E  R  V  S  N  Y  E  D  G

        370        380        390        400        410        420
GGAGTCCTTACCGTTAAACAAGAAACTAGTCTGGAGGGAGATTGCATTATTTGCAAAATT
G  V  L  T  V  K  Q  E  T  S  L  E  G  D  C  I  I  C  K  I

        430        440        450        460        470        480
AAAGCACATGGCACTAACTTCCCCGCAGATGGTCCGGTGATGCAAAAACGGACCAATGGA
K  A  H  G  T  N  F  P  A  D  G  P  V  M  Q  K  R  T  N  G

        490        500        510        520        530        540
TGGGAGCCATCAACTGAAACGGTTATTCCACGGGGTGGAGGAATTCTGATGCGCGATGTG
W  E  P  S  T  E  T  V  I  P  R  G  G  G  I  L  M  R  D  V

        550        560        570        580        590        600
CCCGCACTGAAGCTGCTTGGTAACAAAGGACATCTTCTCTGCGTCATGGAAACAACTTAC
P  A  L  K  L  L  G  N  K  G  H  L  L  C  V  M  E  T  T  Y

        610        620        630        640        650        660
AAGTCAAAAAAAAAAGGTGAACCTGCCAAACCGCACTTTCATCATTTGAGAATGGAGAAG
K  S  K  K  K  G  E  P  A  K  P  H  F  H  H  L  R  M  E  K

        670        680        690        700        710        720
GATAGTGTTAGTGACGATGAGAAGACCATTGAGCAGCACGAGAATGTGAGGGCAAGCTAC
D  S  V  S  D  D  E  K  T  I  E  Q  H  E  N  V  R  A  S  Y

        730        740        750        760        770        780
TTCAATGATAGTGGAAAATGATCATTTCCTTATTGATTTCAATGTTAGGGCATTCAGTTT
F  N  D  S  G  K  *

        790        800        810        820        830        840
CCAAATTTTCTTAGACACAGTCTTTTCCTTTAGCTTCGTAGCCTACTTACCCATGTTTTG

        850        860
TTGAAGTCAATAAATAGCTAAGCACTAC (SEQ ID NOS: 01 & 02)
```

FIG. 9

Green fluorescent protein from *Dendronephthya sp.* dendGFP

```
          10         20         30         40         50         60
5'CATATCGAGAAAGTTGTGAAACCAAATTCTTACTCTACTTTTACTACCATGAATCTGATT
                                                    M  N  L  I

          70         80         90        100        110        120
AAAGAAGATATGAGGGTTAAGGTGCATATGGAAGGGAATGTAAACGGGCATGCTTTTGTG
K  E  D  M  R  V  K  V  H  M  E  G  N  V  N  G  H  A  F  V

         130        140        150        160        170        180
ATTGAAGGGGAAGGAAAAGGAAGGCCCTACGAAGGGACACAGACCTTGAACCTGACAGTG
I  E  G  E  G  K  G  R  P  Y  E  G  T  Q  T  L  N  L  T  V

         190        200        210        220        230        240
AAAGAAGGCGCGCCTCTCCCATTTTCTTACGACATCTTGACAACAGCATTGCACTACGGA
K  E  G  A  P  L  P  F  S  Y  D  I  L  T  T  A  L  H  Y  G

         250        260        270        280        290        300
AACAGAGTATTCACTGAATACCCAGCAGATATCACGGATTATTTCAAGCAATCATTTCCT
N  R  V  F  T  E  Y  P  A  D  I  T  D  Y  F  K  Q  S  F  P

         310        320        330        340        350        360
GAAGGATATTCCTGGGAAAGAACCATGACTTATGAAGACAAGGGCATTTGTACCATCAGA
E  G  Y  S  W  E  R  T  M  T  Y  E  D  K  G  I  C  T  I  R

         370        380        390        400        410        420
AGCGACATAAGCTTGGAAGGTGACTGCTTTTTCCAAAACATTCGTTTTAATGGGATGAAC
S  D  I  S  L  E  G  D  C  F  F  Q  N  I  R  F  N  G  M  N

         430        440        450        460        470        480
TTTCCCCCAAATGGTCCAGTTATGCAGAAGAAAACTTTGAAGTGGGAACCATCCACAGAG
F  P  P  N  G  P  V  M  Q  K  K  T  L  K  W  E  P  S  T  E

         490        500        510        520        530        540
AAGCTGCACGTGCGTGATGGGTTGCTTGTCGGTAATATTAACATGGCTCTGCTGCTTGAA
K  L  H  V  R  D  G  L  L  V  G  N  I  N  M  A  L  L  L  E

         550        560        570        580        590        600
GGAGGTGGACATTACCTGTGTGACTTCAAAACTACTTACAAAGCGAAGAAGGTTGTTCAG
G  G  G  H  Y  L  C  D  F  K  T  T  Y  K  A  K  K  V  V  Q

         610        620        630        640        650        660
TTGCCAGATTATCATTTTGTGGACCATCGCATTGAGATCTTGAGTAATGACAGCGATTAC
L  P  D  Y  H  F  V  D  H  R  I  E  I  L  S  N  D  S  D  Y

         670        680        690        700        710        720
AACAAAGTGAAGCTGTACGAGCATGGGGTTGCTCGCTATTCTCCGTTGCCCAAGTCAGGC
N  K  V  K  L  Y  E  H  G  V  A  R  Y  S  P  L  P  K  S  G

         730        740        750        760        770        780
CTGGTAGAGGTTCAAGGGAAAGCCATAATGACTGCATAGATAAACATGTAGTGAAGACCA
L  V  E  V  Q  G  K  A  I  M  T  A  *

         790        800        810        820        830        840
CATACTCGGGATTAGAGTTTAGGGATTGGTAGTTGTGGTAGATTCTAGCCTACAAATTTT


TTGGG 3' (SEQ ID NO:03 & 04)
```

FIG. 10

Red fluorescent protein from *Zoanthus sp.* zoanRFP

```
         10         20         30         40         50         60
GAGTTGAGTTCTCGACTTCAGTTGTATCACTTTTGACGTATCAAGTGATCTATTCTCAAC

         70         80         90        100        110        120
ATGGCCCATTCAAAGCACGGACTAACAGATGACATGACAATGCATTTCCGTATGGAAGGG
M  A  H  S  K  H  G  L  T  D  D  M  T  M  H  F  R  M  E  G

        130        140        150        160        170        180
TGCGTCGATGGACATAAGTTTGTAATCGAGGGCAACGGCAATGGAAATCCTTTCAAAGGG
C  V  D  G  H  K  F  V  I  E  G  N  G  N  G  N  P  F  K  G

        190        200        210        220        230        240
AAACAGTTTATTAATCTGTGTGTGATTGAAGGAGGACCACTGCCATTCTCCGAAGACATA
K  Q  F  I  N  L  C  V  I  E  G  G  P  L  P  F  S  E  D  I

        250        260        270        280        290        300
TTGTCTGCTGCGTTTGACTACGGAAACAGGCTCTTCACTGAATATCCTGAAGGCATAGTT
L  S  A  A  F  D  Y  G  N  R  L  F  T  E  Y  P  E  G  I  V

        310        320        330        340        350        360
GACTATTTCAAGAACTCGTGTCCTGCTGGATATACGTGGCACAGGTCTTTTCGCTTTGAA
D  Y  F  K  N  S  C  P  A  G  Y  T  W  H  R  S  F  R  F  E

        370        380        390        400        410        420
GATGGAGCAGTTTGCATATGCAGTGCAGATATAACAGTAAATGTTAGGGAAAACTGCATT
D  G  A  V  C  I  C  S  A  D  I  T  V  N  V  R  E  N  C  I

        430        440        450        460        470        480
TATCATGAGTCCACGTTTTATGGAGTGAACTTTCCTGCTGATGGACCTGTGATGAAAAAG
Y  H  E  S  T  F  Y  G  V  N  F  P  A  D  G  P  V  M  K  K

        490        500        510        520        530        540
ATGACAACTAATTGGGAACCGTCCTGCGAGAAAATCATACCAATAAATAGTCAGAAGATA
M  T  T  N  W  E  P  S  C  E  K  I  I  P  I  N  S  Q  K  I

        550        560        570        580        590        600
TTAAAAGGGGATGTCTCCATGTACCTCCTTCTGAAGGATGGTGGGCGTTACCGCTGCCAG
L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G  R  Y  R  C  Q

        610        620        630        640        650        660
TTTGACACAATTTACAAAGCAAAGACTGAGCCAAAAGAAATGCCGGACTGGCACTTCATC
F  D  T  I  Y  K  A  K  T  E  P  K  E  M  P  D  W  H  F  I

        670        680        690        700        710        720
CAGCATAAGCTCAACCGTGAAGACCGCAGCGATGCTAAGAATCAGAAATGGCAACTGATA
Q  H  K  L  N  R  E  D  R  S  D  A  K  N  Q  K  W  Q  L  I

        730        740        750        760        770        780
GAACATGCTATTGCATCCCGATCTGCTTTACCCTGATAACAAAGGAGTTGCTATTGCATG
E  H  A  I  A  S  R  S  A  L  P  *

        790        800        810        820        830        840
TGCATGCCTATTACGCTGATAAAAATGTAGTTTTAACATGCAATTGTATGTGCATGCACA

        850
TTACCCTGATA
```

(SEQ ID NOS:05 & 06)

FIG. 11

Green fluorescent protein from *Scolymia cubensis* scubGFP1 (AY037767)

```
          10         20         30         40         50         60
5'TGTGACATTCAGTCATATAGGAGCCTCTATCGGAGCTGAGGTCCCATTCACCGTTGTGAT
          70         80         90        100        110        120
TTGGACGGGAGCAGATCGAGAACAACMAGGGCTGTACGAGTCTGATAATTTACTTTACAT
         130        140        150        160        170        180
CTACCAACATGCAGCGTGCTGGGATGAAGGTTAAGGAACATATGAAGATCAAACTGCGTA
           M  Q  R  A  G  M  K  V  K  E  H  M  K  I  K  L  R  M

         190        200        210        220        230        240
TGGGAGGTACTGTAAACGGAAAGCATTTCGCGGTTAATGGGACAGGAGACGGCTACCCTT
  G  G  T  V  N  G  K  H  F  A  V  N  G  T  G  D  G  Y  P  Y

         250        260        270        280        290        300
ATCAGGGAAAACAGATTTTGAAACTTATCGTCGAAGGCAGCGAACCTCTGCCTTTCGCTT
  Q  G  K  Q  I  L  K  L  I  V  E  G  S  E  P  L  P  F  A  F

         310        320        330        340        350        360
TTGATATCTTGTCAGCAGCATTCCAGTATGGCAACAGGGCATTCACCGAATACCCAACAG
  D  I  L  S  A  A  F  Q  Y  G  N  R  A  F  T  E  Y  P  T  E

         370        380        390        400        410        420
AGATAGCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTTCTCCTGGGAACGAA
  I  A  D  Y  F  K  Q  S  F  E  F  G  E  G  F  S  W  E  R  S

         430        440        450        460        470        480
GTTTCACTTTCGAAGATGGGGCCATTTGCGTCGCCACCAACGATATAACGATGGTTGGTG
  F  T  F  E  D  G  A  I  C  V  A  T  N  D  I  T  M  V  G  G

         490        500        510        520        530        540
GTGAGTTTCAGTATGATATTCGATTTGATGGTCTGAACTTCCCTGAAGATGGTCCAGTGA
  E  F  Q  Y  D  I  R  F  D  G  L  N  F  P  E  D  G  P  V  M

         550        560        570        580        590        600
TGCAAAAGAAAACCGTAAAATGGGAGCCATCCACTGAGATAATGTATATGCAAAATGGAG
  Q  K  K  T  V  K  W  E  P  S  T  E  I  M  Y  M  Q  N  G  V

         610        620        630        640        650        660
TGCTGAAGGGTGAGGTTAACATGGCTCTGTTGCTTCAAGACAAAAGCCATTACCGTTGCG
  L  K  G  E  V  N  M  A  L  L  L  Q  D  K  S  H  Y  R  C  D

         670        680        690        700        710        720
ACCTCAAAACTACTTACAAAGCTAAGAATAATGTGCCGCATCCTCCAGGCTACCACTATG
  L  K  T  T  Y  K  A  K  N  N  V  P  H  P  P  G  Y  H  Y  V

         730        740        750        760        770        780
TGGATCACTGCATTGAAATACTCGAAGAACGTAAGGATCACGTTAAGCTGCGGGAGCATG
  D  H  C  I  E  I  L  E  E  R  K  D  H  V  K  L  R  E  H  A

         790        800        810        820        830        840
CTAAAGCTCGTTCTAGCCTGTCACCTACCAGTGCAAAAGAACGAAAGGCTTAGGTGATAG
  K  A  R  S  S  L  S  P  T  S  A  K  E  R  K  A  *

         850        860        870        880        890        900
TCAAAAAGACAACAAGACGAAAATGAAAGGTGTTCATTGTTAGAATTTGATATTTTCGAT
         910        920        930        940        950        960
TCAATGATTCGTTAAGGGATTTGCTAGAGGCTAGCTAACAGGTTAACATCATAAGGATAG
         970        980        990       1000       1010       1020
AGATTYCGTTGCGGAGTTAGAACCTTWATATTTTCCGAATTCCAMCTAGAGTCGTTGAGA
        1030       1040       1050       1060       1070       1080
AATTTATTAGAGACTAGCTTTAGAGTTACTTTTGTGGAAAAAAAGGTTTCCATTTTTTGC
        1090       1100       1110       1120       1130       1140
GTTATTACAGCATTTAAAGCATAGGAATAGAGATTCGGTTATGGAAAATAACAGTAGGAA
        1150       1160       1170
AATACGTTGTGAAAATAAACTTGTTGTCGAAAAAAAAA 3'
```

(SEQ ID NOS:07&08)

FIG. 12

Green fluorescent protein from *Scolymia cubensis* scubGFP2 (AY037771)

```
          10         20         30         40         50         60
5'CCTGGTGATTTGGACGAGAGCAGATCGAGAATAGCAAGGTTTTACCAGCGTGATAATTTA
          70         80         90        100        110        120
CTTTACATCTAACAACATGCAATCTGCTGGGAAGAAGAATGTCGTTAAGGACTTCATGAA
                  M  Q  S  A  G  K  K  N  V  V  K  D  F  M  K

        130        140        150        160        170        180
GATCACACTGCGTATGGACGGTGCTGTAAACGGGAAGCCCTTCGCGGTTAATGGAACAGG
 I  T  L  R  M  D  G  A  V  N  G  K  P  F  A  V  N  G  T  G

        190        200        210        220        230        240
AGATGGCAACCCTTATGGTGGAATACAGAGTTTGAAGCTTACCGTCGATGGCAACAAACC
 D  G  N  P  Y  G  G  I  Q  S  L  K  L  T  V  D  G  N  K  P

        250        260        270        280        290        300
TCTGCCTTTTGCTTTTGATATCTTGTCAGCAGCATTCCAGTATGGCAACAGGGCATTCAC
 L  P  F  A  F  D  I  L  S  A  A  F  Q  Y  G  N  R  A  F  T

        310        320        330        340        350        360
CGAATACCCAAAAGAGATATCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTT
 E  Y  P  K  E  I  S  D  Y  F  K  Q  S  F  E  F  G  E  G  F

        370        380        390        400        410        420
TACCTGGGAACGAAGTTTCACTTTCGAAGACGGGGCCATTTGCGTCGCCACGAACGATAT
 T  W  E  R  S  F  T  F  E  D  G  A  I  C  V  A  T  N  D  I

        430        440        450        460        470        480
AAAGATGGTTGGCGATGAGTTTCAATATAACATTCGATTTGATGGTGTGAATTTCCCTGA
 K  M  V  G  D  E  F  Q  Y  N  I  R  F  D  G  V  N  F  P  E

        490        500        510        520        530        540
AGATGGTCCWGTYATGCAGAAGAAAACGGTGAAGTGGGAGCCATCCACAGAGATAATGCG
 D  G  P  V  M  Q  K  K  T  V  K  W  E  P  S  T  E  I  M  R

        550        560        570        580        590        600
TGTGCAAGGTGGAGTGCTAAAGGGTGAGGTTAACATGGCTCTGTTGCTTAAAGACAAAAG
 V  Q  G  G  V  L  K  G  E  V  N  M  A  L  L  L  K  D  K  S

        610        620        630        640        650        660
CCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAATCCTGTCCCGCCGACGGC
 H  Y  R  C  D  F  K  T  T  Y  K  A  K  N  P  V  P  P  T  A

        670        680        690        700        710        720
GCTTCCAGACTACCACTATGTGGATCACTGTATTGAAATCACCGAGGAAAATAGGGATTA
 L  P  D  Y  H  Y  V  D  H  C  I  E  I  T  E  E  N  R  D  Y

        730        740        750        760        770        780
CGTTAAGCTGCAGGAGTATGCTAAAGCTCGTTCTGGCCTGCACCTGCCCGAACTGCAAAA
 V  K  L  Q  E  Y  A  K  A  R  S  G  L  H  L  P  E  L  Q  K

        790        800        810
GTAAAGGCTTAGGCGATAGTCAAGACGACAACGAGAAGA 3'
 *
```

(SEQ ID NO:09 & 10)

FIG. 13

Red fluorescent protein from *Ricordea florida* rfloRFP (AY037773)

```
          10         20         30         40         50         60
5'TGTGAAAGTTAACATTTTACTTTACTTCTACCAGCATGAGTGCACTCAAAGAGGAAATGA
                                        M  S  A  L  K  E  E  M  K

          70         80         90        100        110        120
AAATCAAGCTTACATTGGTGGGCGTTGTTAACGGGCACCCATTCAAGATCATTGGGGACG
  I  K  L  T  L  V  G  V  V  N  G  H  P  F  K  I  I  G  D  G

         130        140        150        160        170        180
GAAAAGGCAAACCCTATGAGGGATCGCAGGAATTAACCCTTGCCGTGGTGGAAGGAGGGC
  K  G  K  P  Y  E  G  S  Q  E  L  T  L  A  V  V  E  G  G  P

         190        200        210        220        230        240
CTCTGCCTTTCTCTTATGATATCCTGACAACGATAGTTCACTATGGCAACAGGGCATTTG
  L  P  F  S  Y  D  I  L  T  T  I  V  H  Y  G  N  R  A  F  V

         250        260        270        280        290        300
TGAACTACCCAAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGGTGCTG
  N  Y  P  K  D  I  P  D  I  F  K  Q  T  C  S  G  P  G  A  G

         310        320        330        340        350        360
GATATTCCTGGCAAAGGACCATGAGTTTTGAAGACGGAGGCGTTTGCACTGCTACGAGCC
  Y  S  W  Q  R  T  M  S  F  E  D  G  G  V  C  T  A  T  S  H

         370        380        390        400        410        420
ATATCAGGGTGGATGGCGACACTTTCAATTATGACATTCACTTCATGGGAGCGGATTTCC
  I  R  V  D  G  D  T  F  N  Y  D  I  H  F  M  G  A  D  F  P

         430        440        450        460        470        480
CTCTTAATGGTCCAGTGATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAA
  L  N  G  P  V  M  Q  K  R  T  V  K  W  E  P  S  T  E  I  M

         490        500        510        520        530        540
TGTTTCAATGTGATGGATTGCTGAGGGGTGATGTTGCCATGTCTCTGTTGCTGAAAGGAG
  F  Q  C  D  G  L  L  R  G  D  V  A  M  S  L  L  L  K  G  G

         550        560        570        580        590        600
GCGGCCATTACCGATGTGACTTTAAAACTATTTATAAACCCAAGAAGAATGTCAAGATGC
  G  H  Y  R  C  D  F  K  T  I  Y  K  P  K  K  N  V  K  M  P

         610        620        630        640        650        660
CAGGTTACCATTTTGTGGACCACTGCATTGAGATAACGAGTCAACAGGACGATTACAACG
  G  Y  H  F  V  D  H  C  I  E  I  T  S  Q  Q  D  D  Y  N  V

         670        680        690        700        710        720
TGGTTGAGCTGTACGAGGGTGCTGTAGCCCACTACTCTCCTCTGCAGAAACCATGCCAAG
  V  E  L  Y  E  G  A  V  A  H  Y  S  P  L  Q  K  P  C  Q  A

         730        740        750        760        770        780
CAAAGGCATAAAGCCAAACAACCCAAGAGGACAACAAGACATTTAATCAAATCACATCTT
  K  A  *

         790        800
TGTATTTTTGGTTAGAGTTGAAAAAAA 3'
```

(SEQ ID NO:11 & 12)

FIG. 14

Green fluorescent protein from *Ricordea florida* rfloGFP (AY037772)

```
          10         20         30         40         50         60
5'AGTCACCTCGGTGTTTTTAGGACAGGAAGGATCACGAGCAAGAGAAGAACTGTGAAAGTT
          70         80         90        100        110        120
  AACACTTTACTCTACTTCTACCAGCATGAGTGCACTCAAAGAGGAAATGAAAATCAAGCT
                               M  S  A  L  K  E  E  M  K  I  K  L

         130        140        150        160        170        180
  TAAAATGGTGGGCGTTGTTAACGGGCAGTCATTTCAGATCGATGGGGAAGGAAAAGGCAA
   K  M  V  G  V  V  N  G  Q  S  F  Q  I  D  G  E  G  K  G  K

         190        200        210        220        230        240
  ACCTTACGAGGGATCACAGAAATTAACCCTTGAAGTGGTGGAAGGAGGGCCTCTGCTCTT
   P  Y  E  G  S  Q  K  L  T  L  E  V  V  E  G  G  P  L  L  F

         250        260        270        280        290        300
  CTCTTATGATATCCTGACAACGATATTTCAGTATGGCAACAGGGCATTCGTGAACTACCC
   S  Y  D  I  L  T  T  I  F  Q  Y  G  N  R  A  F  V  N  Y  P

         310        320        330        340        350        360
  AAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGATGGTGGATTTTCCTG
   K  D  I  P  D  I  F  K  Q  T  C  S  G  P  D  G  G  F  S  W

         370        380        390        400        410        420
  GCAAAGGACCATGACTTATGAAGACGGAGGGGTTTGCACTGCTTCAAACCACATCAGCGT
   Q  R  T  M  T  Y  E  D  G  G  V  C  T  A  S  N  H  I  S  V

         430        440        450        460        470        480
  GGACGGCGACACTTTTTATTATGTGATAAGATTTAATGGAGAGAATTTTCCTCCAAATGG
   D  G  D  T  F  Y  Y  V  I  R  F  N  G  E  N  F  P  P  N  G

         490        500        510        520        530        540
  TCCAGTAATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAATGTTTGAACG
   P  V  M  Q  K  R  T  V  K  W  E  P  S  T  E  I  M  F  E  R

         550        560        570        580        590        600
  TGATGGATTGCTGAGGGGTGACATTGCCATGTCTCTGTTGCTGAAAGGAGGCGGCCATTA
   D  G  L  L  R  G  D  I  A  M  S  L  L  L  K  G  G  G  H  Y

         610        620        630        640        650        660
  CCGATGTGACTTTAAAACTATTTATACACCCAAGAGGAAGGTCAACATGCCAGGTTACCA
   R  C  D  F  K  T  I  Y  T  P  K  R  K  V  N  M  P  G  Y  H

         670        680        690        700        710        720
  TTTTGTGGACCACTGCATTGAGATACAGAAGCACGACAAGGATTACAACATGGCTGTGCT
   F  V  D  H  C  I  E  I  Q  K  H  D  K  D  Y  N  M  A  V  L

         730        740        750        760        770        780
  CTCTGAGGATGCTGTAGCCCACAACTCTCCTCTGGAGAAAAAAAGCCAAGCAAAGGCGTA
   S  E  D  A  V  A  H  N  S  P  L  E  K  K  S  Q  A  K  A  *

         790
  AAGCCAAACAACCTAA 3'
```

(SEQ ID NO:13&14)

FIG. 15

Red fluorescent protein from *Montastraea cavernosa* mcavRFP (AY037770)

```
          10         20         30         40         50         60
5'ACGCAGGGATTCACCCTGGTGATTTGGAAGAGAGCAGACCGAGAACAACAAGAGCTGTAT
          70         80         90        100        110        120
AAGGCTGATATCTTACTTTACGTCTACCATCATGAGTGTGATTAAATCAGTCATGAAGAT
 R  L  I  S  Y  F  T  S  T  I  M  S  V  I  K  S  V  M  K  I

         130        140        150        160        170        180
CAAGCTGCGTATGGAAGGCAGTGTAAACGGGCACAACTTCGTAATTGTTGGAGAAGGAGA
 K  L  R  M  E  G  S  V  N  G  H  N  F  V  I  V  G  E  G  E

         190        200        210        220        230        240
AGGCAAGCCTTATGAGGGAACACAGAGTATGGACCTTACAGTCAAAGAAGGCGCACCTCT
 G  K  P  Y  E  G  T  Q  S  M  D  L  T  V  K  E  G  A  P  L

         250        260        270        280        290        300
GCCTTTCGCCTACGATATCATGACAACAGTATTCCATTACGGCAATAGGGTATTCGCAAA
 P  F  A  Y  D  I  M  T  T  V  F  H  Y  G  N  R  V  F  A  K

         310        320        330        340        350        360
ATACCCAAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGGAGTATTCCTGGGA
 Y  P  K  H  I  P  D  Y  F  K  Q  M  F  P  E  E  Y  S  W  E

         370        380        390        400        410        420
ACGAAGCATGAATTTCGAAGGCGGGGGCATTTGCACCGCCAGGAACGAGATAACAATGGA
 R  S  M  N  F  E  G  G  G  I  C  T  A  R  N  E  I  T  M  E

         430        440        450        460        470        480
AGGCGACTGTTTTTTCAATAAAGTTCGATTTGATGGTGTGAACTTCCCCCCCAATGGTCC
 G  D  C  F  F  N  K  V  R  F  D  G  V  N  F  P  P  N  G  P

         490        500        510        520        530        540
AGTCATGCAGAAGAAGACGCTGAAATGGGAGCCATCCACTGAAAAAATGTATGTGCGTGA
 V  M  Q  K  K  T  L  K  W  E  P  S  T  E  K  M  Y  V  R  D

         550        560        570        580        590        600
TGGAGTGCTGACGGGTGATATCAACATGGCTTTGTTGCTTGAAGGAGGTGGCCATTACCG
 G  V  L  T  G  D  I  N  M  A  L  L  L  E  G  G  G  H  Y  R

         610        620        630        640        650        660
ATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGGGTGTCAAGTTACCAGATTATCA
 C  D  F  R  T  T  Y  R  A  K  K  K  G  V  K  L  P  D  Y  H

         670        680        690        700        710        720
CTTTGAGGATCACTCCATTGAGATTTTGCGCCATGACAAAGAATACACTGAGGTTAAGCT
 F  E  D  H  S  I  E  I  L  R  H  D  K  E  Y  T  E  V  K  L

         730        740        750        760        770        780
GTATGAGCATGCCGAAGCTCATTCTGGGCTGCCGAGGGTGGCAAAGTAAAGGCTTAACGA
 Y  E  H  A  E  A  H  S  G  L  P  R  V  A  K  *

         790
AAAGCCAAGACCACA 3'
```

(SEQ ID NO:15 & 16)

FIG. 16

Green fluorescent protein from *Montastraea cavernosa* mcavGFP (AY037769)

```
          10         20         30         40         50         60
5'ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA
          70         80         90        100        110        120
TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCAG
                     M  T  S  V  A  Q  E  K  G  V  I  K  P  D

        130        140        150        160        170        180
ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG
  M  K  M  K  L  R  M  E  G  A  V  N  G  H  K  F  V  V  E  G

        190        200        210        220        230        240
GAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG
  D  G  K  G  K  P  F  D  G  T  Q  T  M  D  L  T  V  I  E  G

        250        260        270        280        290        300
GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG
  A  P  L  P  F  A  Y  D  I  L  T  T  V  F  D  Y  G  N  R  V

        310        320        330        340        350        360
TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT
  F  A  K  Y  P  E  D  I  A  D  Y  F  K  Q  T  F  P  E  G  Y

        370        380        390        400        410        420
ACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACA
  F  W  E  R  S  M  T  Y  E  D  Q  G  I  C  I  A  T  N  D  I

        430        440        450        460        470        480
TAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTGATGGTGTGA
  T  M  M  E  G  V  D  D  C  F  A  Y  K  I  R  F  D  G  V  N

        490        500        510        520        530        540
ACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACTG
  F  P  A  N  G  P  V  M  Q  R  K  T  L  K  W  E  P  S  T  E

        550        560        570        580        590        600
AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTG
  I  M  Y  A  R  D  G  V  L  K  G  D  V  N  M  A  L  L  L  E

        610        620        630        640        650        660
AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCC
  G  G  G  H  Y  R  C  D  F  K  T  T  Y  K  A  K  K  V  V  R

        670        680        690        700        710        720
GGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT
  L  P  D  Y  H  F  V  D  H  R  I  E  I  V  S  H  D  K  D  Y

        730        740        750        760        770        780
ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA
  N  K  V  K  L  H  E  H  A  E  A  R  H  G  L  S  R  K  A  K

        790        800        810        820        830        840
AGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTTGTTA
  *

        850        860        870        880        890        900
AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTCCG
        910        920        930        940        950        960
GGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTTT
        970        980        990       1000       1010       1020
TGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTTGTGGTCAAATGCAAGTAAG
       1030       1040       1050       1060
AAAACTGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAAAAAA 3'
```

(SEQ ID NOS: 17 & 18)

FIG. 17

Green fluorescent protein from *Condylactis gigantea* cgigGFP (AY037776)

```
          10         20         30         40         50         60
5'ACAGCTGTTCATCCACGCTCATTCAAGACGCCGTCAACTTTATTCCAGTCAGGAAAATGT
                                                      M  Y

          70         80         90        100        110        120
ATCCTTGGATCAAGGAAACCATGCGCAGTAAGGTTTACATGGAAGGAGATGTTAACAACC
  P  W  I  K  E  T  M  R  S  K  V  Y  M  E  G  D  V  N  N  H

         130        140        150        160        170        180
ACGCCTTCAAGTGCACTGCAGTAGGAGAAGGAAAACCATACAAAGGCTCACAAGACCTGA
  A  F  K  C  T  A  V  G  E  G  K  P  Y  K  G  S  Q  D  L  T

         190        200        210        220        230        240
CGATTACCGTCACTGAAGGAGGTCCTCTGCCATTTGCTTTCGACATTCTTTCACACGCCT
  I  T  V  T  E  G  G  P  L  P  F  A  F  D  I  L  S  H  A  F

         250        260        270        280        290        300
TTCAGTATGGCAACAAGGTGTTCACCGATTACCCCGACGATATTCCTGATTTCTTTAAGC
  Q  Y  G  N  K  V  F  T  D  Y  P  D  D  I  P  D  F  F  K  Q

         310        320        330        340        350        360
AGTCTCTCTCGGATGGTTTTACTTGGAGAAGAGTAAGCACSTATGACGATGGAGGAGTCC
  S  L  S  D  G  F  T  W  R  R  V  S  T  Y  D  D  G  G  V  L

         370        380        390        400        410        420
TCACAGTTACCCAAGACACTAGTCTGAAGGGAGATTGCATTATTTGCAACATTAAAGTCC
  T  V  T  Q  D  T  S  L  K  G  D  C  I  I  C  N  I  K  V  H

         430        440        450        460        470        480
ATGGCACTAACTTCCCCGAAAATGGTCCGGTGATGCAAAACAAGACCGATGGATGGGAGC
  G  T  N  F  P  E  N  G  P  V  M  Q  N  K  T  D  G  W  E  P

         490        500        510        520        530        540
CATCCAGCACTGAAACGGTTATTCCACAAGATGGAGGAATTGTTGCTGCGCGATCACCCG
  S  S  T  E  T  V  I  P  Q  D  G  G  I  V  A  A  R  S  P  A

         550        560        570        580        590        600
CACTAAGGCTGCGTGATAAAGGTCATCTTATCTGCCACATGGAAACAACTTACAAGCCAA
  L  R  L  R  D  K  G  H  L  I  C  H  M  E  T  T  Y  K  P  N

         610        620        630        640        650        660
ACAAAGAGGTGAAGCTGCCAGAACTCCACTTTCATCATTTGCGAATGGAAAAGCTGAGTG
  K  E  V  K  L  P  E  L  H  F  H  H  L  R  M  E  K  L  S  V

         670        680        690        700        710        720
TTAGTGACGATGGGAAGACCATTAAGCAGCACGAGTATGTGGTGGCTAGCTACTCCAAAG
  S  D  D  G  K  T  I  K  Q  H  E  Y  V  V  A  S  Y  S  K  V

         730        740        750        760        770        780
TGCCTTCGAAGATAGGACGTCAATGATCATTTCCCTTATTAAATATCAATGATGTGGCTT
  P  S  K  I  G  R  Q  *

         790        800        810        820        830        840
TCAATTTTCCAAAATTTTGTTAAGACATAGGTCTTTTGGATTTTTGGTAACCCCAACCTT
         850        860        870        880        890
AATTCCCAATAATTTTTGTTGGAAAGTCAAATAAAACCAGCCTTCCCTGGGCCTTTAA 3'
```

(SEQ ID NOS: 19 & 20)

FIG. 18

Green fluorescent protein from *Agaricia fragilis* afraGFP (AY037765)

```
          10         20         30         40         50         60
5'CAAGGAAGCCAAATCTTTTACCAGAGATCTCGCGTGAAAGCAACCTATGAGTGATGGCGA
                                                     M  A  I

          70         80         90        100        110        120
TTTCTACTCTAAAGAACGTCATCATCATCGTTATTATATACTCCTGCAGCACTTGTGCTG
  S  T  L  K  N  V  I  I  I  V  I  I  Y  S  C  S  T  C  A  V

         130        140        150        160        170        180
TTTGGTCGAATTCAAACTCTGAATCCTCTTTCACTAATGGGATTGCAGAGGAAATGAAGA
  W  S  N  S  N  S  E  S  S  F  T  N  G  I  A  E  E  M  K  T

         190        200        210        220        230        240
CTAGGGTACATTTGGAGGGTACTGTTAACGGGCACTCCTTTACAATTAAAGGCGAAGGAA
  R  V  H  L  E  G  T  V  N  G  H  S  F  T  I  K  G  E  G  R

         250        260        270        280        290        300
GAGGCTACCCTTACAAAGGAGAACAGTTTATGAGCCTTGAGGTCGTCAATGGTGCTCCTC
  G  Y  P  Y  K  G  E  Q  F  M  S  L  E  V  V  N  G  A  P  L

         310        320        330        340        350        360
TGCCGTTCTCTTTTGATATCTTGACACCAGCATTTATGTATGGCAACAGAGTGTTCACCA
  P  F  S  F  D  I  L  T  P  A  F  M  Y  G  N  R  V  F  T  K

         370        380        390        400        410        420
AGTACCCACCAAACATACCAGACTATTTCAAGCAGACGTTTCCTGAAGGGTATCACTGGG
  Y  P  P  N  I  P  D  Y  F  K  Q  T  F  P  E  G  Y  H  W  E

         430        440        450        460        470        480
AAAGAAACATTCCCTTTGAAGATCAGGCCGCGTGCACGGTAACCAGCCACATAAGATTGG
  R  N  I  P  F  E  D  Q  A  A  C  T  V  T  S  H  I  R  L  E

         490        500        510        520        530        540
AAGAGGAAGAGAGGCGTTTTGTAAATAACGTCAGATTTCACTGTGTGAACTTTCCCCCTA
  E  E  E  R  R  F  V  N  N  V  R  F  H  C  V  N  F  P  P  N

         550        560        570        580        590        600
ATGGTCCAGTCATGCAGAGGAGGATACTGAAATGGGAGCCATCCACTGAGAACATTTATC
  G  P  V  M  Q  R  R  I  L  K  W  E  P  S  T  E  N  I  Y  P

         610        620        630        640        650        660
CGCGTGATGGGTTTCTGGAGGGCCATGTTGATATGACTCTTCGGGTTGAAGGAGGTGGCT
  R  D  G  F  L  E  G  H  V  D  M  T  L  R  V  E  G  G  G  Y

         670        680        690        700        710        720
ATTACCGAGCTGAGTTCAAAAGTACTTACAAAGGGAAGACCCCAGTCCGCGACATGCCAG
  Y  R  A  E  F  K  S  T  Y  K  G  K  T  P  V  R  D  M  P  D

         730        740        750        760        770        780
ACTTTCACTTCATAGACCACCGCATTGAGATTACGGAGCATGACGAAGACTACACCAATG
  F  H  F  I  D  H  R  I  E  I  T  E  H  D  E  D  Y  T  N  V

         790        800        810        820        830        840
TTGAGCTGCATGACGTATCCTGGGCTCGTTACTCTATGCTGCCGACTATGTAAGCGGAAA
  E  L  H  D  V  S  W  A  R  Y  S  M  L  P  T  M

         850        860        870        880        890        900
AGGCAAGGCAACAAGACGCAAAACCGCCCTGTTTGTCTCTTTTCATAAGAGATTTGACAA
         910        920        930        940        950        960
CCGTGGTTCTTTGCCATTTAATTTGAATTAGTTTAAATTAAATCTTTGGGATTGATGTAG
         970        980        990       1000       1010       1020
ACGCTTTGGTTGCTAAGTAAGAAAACATTTGTGATTATTAAATTTGTTGCCTGAAGCAAA
       1030
AAAAAAAAAA 3'
```

(SEQ ID NOS:21 & 22)

FIG. 19

Green fluorescent protein from *Ricordea florida* rfloGFP2 (AY037774)

```
          10         20         30         40         50         60
5'AGCCACTTCGGTGTCTTGTCGAGAGGAAGGATCACGAACAAGAGAAGAGCTGTAAAAGTT
          70         80         90        100        110        120
  AAAATTTTACTTTACTTCTTCCAGCATGAATGCACTTCAAGAGGAAATGAAAATCAAGCT
                              M  N  A  L  Q  E  E  M  K  I  K  L

        130        140        150        160        170        180
  TACAATGGTGGGCGTTGTTAACGGGCAGTCATTTAAGATCGATGGGAAAGGAAAAGGGAA
   T  M  V  G  V  V  N  G  Q  S  F  K  I  D  G  K  G  K  G  K

        190        200        210        220        230        240
  ACCTTACGAGGGATCACAGGAATTGACCCTTAAAGTGGTGGAAGGCGGGCCTCTGCTCTT
   P  Y  E  G  S  Q  E  L  T  L  K  V  V  E  G  G  P  L  L  F

        250        260        270        280        290        300
  CTCTTATGATATCCTGACAACGATATTTCAGTATGGCAACAGGGCATTCGTGAACTACCC
   S  Y  D  I  L  T  T  I  F  Q  Y  G  N  R  A  F  V  N  Y  P

        310        320        330        340        350        360
  AAAGGACATACCAGATATTTTCAAGCAAACGTGTTCTGGTCTTGATGGCGGATATTCGTG
   K  D  I  P  D  I  F  K  Q  T  C  S  G  L  D  G  G  Y  S  W

        370        380        390        400        410        420
  GCAAAGGACCATGACTTATGAGGACGGAGGGGTTTGTACTGCTACAAGCAACGTCAGCGT
   Q  R  T  M  T  Y  E  D  G  G  V  C  T  A  T  S  N  V  S  V

        430        440        450        460        470        480
  GGTCGGCGACACTTTCAATTATGAAATTCACTTTATGGGGGCGAATTTTCCTCCAAATGG
   V  G  D  T  F  N  Y  E  I  H  F  M  G  A  N  F  P  P  N  G

        490        500        510        520        530        540
  TCCRGTGATGCAGAAAAGAACAGTGAAGTGGGAGCCCTCCACTGAGATAATGTTTGAACG
   P  V  M  Q  K  R  T  V  K  W  E  P  S  T  E  I  M  F  E  R

        550        560        570        580        590        600
  TGATGGATTGCTGAGGGGTGATGTTCCCATGTCTCTGTTGCTGAAAGGAGGCGACCATTA
   D  G  L  L  R  G  D  V  P  M  S  L  L  L  K  G  G  D  H  Y

        610        620        630        640        650        660
  CCGATGTGACTTTAAAACTATTTATAAACCCAACAAGAAGGTCAAGCTGCCAGGTTACCA
   R  C  D  F  K  T  I  Y  K  P  N  K  K  V  K  L  P  G  Y  H

        670        680        690        700        710        720
  TTTTGTGGACCACTGCATTGAGATAAAGAGTCAAGAGAATGATTACAACATGGTTGCGCT
   F  V  D  H  C  I  E  I  K  S  Q  E  N  D  Y  N  M  V  A  L

        730        740        750        760        770        780
  CTTTGAGGATGCTGTAGCACACTACTCTCCTCTGGAGAAAAAGAGCCAGGCAAAGGCGTA
   F  E  D  A  V  A  H  Y  S  P  L  E  K  K  S  Q  A  K  A  *

        790        800        810        820        830        840
  AATCCAAACAACCTAAGAAGACGACAAGGCATTCAATCTAATCGCATGTTTGAATTTTTG
        850        860        870        880        890        900
  GTTAGGAATGTGTTGGGTCAGACTAGGTCTAGAACGTTTCATTTTGGCTGGATTTGTTTT
        910        920        930        940        950        960
  ACTCAGTTATAGACAAGAAAAAAATCTTAAATGACTTGGGTTGGATTTAGCTTTCGGCAC
        970        980        990       1000       1010       1020
  TGTCAATTCCGGATTCCTTAGAAATATTTGAGACCAAGCCTTTTTTTGAGCTGAGAACGT

  AATC 3'
```

(SEQ ID NOS: 23 & 24)

FIG. 20

Green fluorescent protein from *Montastraea cavernosa* mcavGFP2 (AY037768)

```
          10         20         30         40         50         60
5'AGAGCTGTAGGGTGATATCTTACTTACGTCTACCATCATGACCAGTGTTGCACAGGAAAA
                                          M  T  S  V  A  Q  E  K

          70         80         90        100        110        120
GGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCA
 G  V  I  K  P  D  M  K  M  K  L  R  M  E  G  A  V  N  G  H

         130        140        150        160        170        180
CAAGTTCGTGATTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGA
 K  F  V  I  E  G  D  G  K  G  K  P  F  D  G  T  Q  T  M  D

         190        200        210        220        230        240
CCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGCTATCTTGACAACAGTATT
 L  T  V  I  E  G  A  P  L  P  F  A  Y  A  I  L  T  T  V  F

         250        260        270        280        290        300
CGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCA
 D  Y  G  N  R  V  F  A  K  Y  P  E  D  I  A  D  Y  F  K  Q

         310        320        330        340        350        360
GACATTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTG
 T  F  P  E  G  Y  F  W  E  R  S  M  T  Y  E  D  Q  G  I  C

         370        380        390        400        410        420
CATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAAAT
 I  A  T  N  D  I  T  M  M  K  G  V  D  D  C  F  V  Y  K  I

         430        440        450        460        470        480
TCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAA
 R  F  D  G  V  N  F  P  A  N  G  P  V  M  Q  R  K  T  L  K

         490        500        510        520        530        540
ATGGGAGCCATCCACTGAGAAAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAA
 W  E  P  S  T  E  K  M  Y  A  R  D  G  V  L  K  G  D  V  N

         550        560        570        580        590        600
CATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAG
 M  A  L  L  L  E  G  G  G  H  Y  R  C  D  F  K  T  T  Y  R

         610        620        630        640        650        660
AGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTGGACCATCGCATTGAGATTGT
 A  K  K  V  V  Q  L  P  D  Y  H  F  V  D  H  R  I  E  I  V

         670        680        690        700        710        720
GAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGG
 S  H  D  K  D  Y  N  K  V  K  L  Y  E  H  A  E  A  H  S  G

         730        740        750        760        770        780
GCTGCCGAGGCAGGCCAAGTAAAGGCTTAATGAAAAGCCAAGACGACAACAAGGAGAAAC
 L  P  R  Q  A  K  *

         790        800        810        820        830        840
AAAGTATTTTTTTTGTTAAATTTCAAGGCATTTACTCGGAATTAGTATTTGATACTTTCG
         850        860        870        880        890        900
ATTCAAGGATTTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTTGTATTTTGTGAAAA
         910
AAAGATAGTTTCC 3'
```

(SEQ ID NOS: 25 & 26)

FIG. 21

Green fluorescent protein homolog from *Montastraea annularis* mannFP (AY037766)

```
          10         20         30         40         50         60
5'TGGTTAACGCAGAGTCGCGGGGGGTTCCTGGCTAATAATTGATTCTATTTTGGGTGTGAC
          70         80         90        100        110        120
ATTCAGGTTTAAAGCAGCATCCTCAGTGCTGAGGTCTCATTCACCCTGGTGATTTGGAAG
         130        140        150        160        170        180
AGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAAAATCTTACTTGCCTCTACCACC
         190        200        210        220        230        240
ATGAGTATGATTAAACCAGAAATGAAGATCAAGATGCGTATGGACGGTGCTGTAAACGGG
M  S  M  I  K  P  E  M  K  I  K  M  R  M  D  G  A  V  N  G

         250        260        270        280        290        300
CACAAGTTCGTGATTACAGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAAACAGACTATG
H  K  F  V  I  T  G  E  G  S  G  E  P  F  E  G  K  Q  T  M

         310        320        330        340        350        360
AACCTGACAGTCATAGACGGCGGACCTCTGCCTTTCGCTTTCGACATCTTGACAACAGCA
N  L  T  V  I  D  G  G  P  L  P  F  A  F  D  I  L  T  T  A

         370        380        390        400        410        420
TTCGATTACGGCAMCAGGGTATTCGCCAAATACCCAGAAGACATCCCAGACTATTTCAAG
F  D  Y  G  X  R  V  F  A  K  Y  P  E  D  I  P  D  Y  F  K

         430        440        450        460        470        480
CAGTCGTTTCCTGAGGGGTTTTCTTGGGAACGAAGCATGACTTACGAAGACGGGGGCATT
Q  S  F  P  E  G  F  S  W  E  R  S  M  T  Y  E  D  G  G  I

         490        500        510        520        530        540
TGCATCGCCACAAATGACATAAAAATGGAAGGCGACTGCTTTTCCTATGAAATTCGATTT
C  I  A  T  N  D  I  K  M  E  G  D  C  F  S  Y  E  I  R  F

         550        560        570        580        590        600
GATGGGGTGAACTTTCCTGCCAATAGTCCAGTTATGCAGAAGAAGACCGTGAAATGGGAG
D  G  V  N  F  P  A  N  S  P  V  M  Q  K  K  T  V  K  W  E

         610        620        630        640        650        660
CCATGCACTGRGGAAATGTATGTGCGTGATGGAGTGCTTAAAGGTGGTCTTAACATGGCT
P  C  T  X  E  M  Y  V  R  D  G  V  L  K  G  G  L  N  M  A

         670        680        690        700        710        720
CTGTTGCTTGAAGGAGGTGGCCATTTCCGATGTGACTTGAAAACTACTTACAAAGCTAAG
L  L  L  E  G  G  G  H  F  R  C  D  L  K  T  T  Y  K  A  K

         730        740        750        760        770        780
AAGGTTGTCCAGATGCCAGACTATCACTTTGTGAATCACCGACTTGAGATAACATGGCAT
K  V  V  Q  M  P  D  Y  H  F  V  N  H  R  L  E  I  T  W  H

         790        800        810        820        830        840
GACGAGGATTACAACAATGTTAAGCTGTCTGAGCATGCAGAAGCTCATTCTGGACTGCCA
D  E  D  Y  N  N  V  K  L  S  E  H  A  E  A  H  S  G  L  P

         850        860        870        880        890        900
AGGCAGGCCAAATAAAGGCTTGACGAAAAGCCAAAACGGCAAAGAGTACAAGAAAGTATA
R  Q  A  K  *

         910        920        930        940        950        960
TATAAATGTATATTTTTCAACTGAAAGGCATTCCACTCGGAATTAGTATTTGATACTTTC
         970        980        990       1000       1010       1020
AATTCAAGGATTTATTTTGGGATTTGCTAGCCACTAGCTTTATTGTTAAATTAAGTTAAA
        1030       1040       1050       1060       1070       1080
GACGGTTTAGCATTTTTTCGGTATTACAACATAGGCACAGACGTCTTAACCCCAGTAGTG
        1090       1100       1110       1120       1130
GTCAGGTACAAGTAAGAAAACTTTGGTGAGAATAGACTTGTAGTCGAAAAAAA 3'
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(SEQ ID NOS:27 & 28)